SEQUENCE LISTING

<110> Meyers, Rachel A.
     MacBeth, Kyle J.

<120> 14094, A NOVEL TRYPSIN FAMILY MEMBER AND
  USES THEREFOR

<130> 10448-046002

<150> US 09/633,300
<151> 2000-08-08

<150> US 60/200,621
<151> 2000-04-28

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (628)...(1986)

<221> misc_feature
<222> (1)...(2948)
<223> n = A,T,C or G

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gtatttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact   180
gttacccact ttgcctcgtc ttcaccctgt ccaaacaccg gtctccaatt tgcccttcag   240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca   300
ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc   360
caaactccaa aaaaaaaccg gaattcagcc tggttaagtc caagctgaat tccgggtggg   420
ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattaggtc atgcccgtat   480
gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc   540
gtggtgccat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg   600
gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt   654
                                   Met Gly Glu Asn Asp Pro Pro Ala Val
                                   1   5

gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa   702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10   15   20   25

ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg   750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
            30   35   40

```
tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att      798
Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
            45                  50                  55

gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc      846
Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys
        60                  65                  70

tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata      894
Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile
        75                  80                  85

gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac      942
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
90              95                  100                 105

cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca      990
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr
                110                 115                 120

gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac     1038
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr
            125                 130                 135

gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca     1086
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser
        140                 145                 150

gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt     1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe
        155                 160                 165

gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac     1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His
170                 175                 180                 185

cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc     1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr
                190                 195                 200

ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc     1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile
            205                 210                 215

gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc     1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser
        220                 225                 230

ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc     1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro
        235                 240                 245

ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc     1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro
250                 255                 260                 265

aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca     1470
```

```
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro
            270             275             280
```

```
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag    1518
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys
            285             290             295
```

```
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca    1566
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro
            300             305             310
```

```
ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa    1614
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
            315             320             325
```

```
gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc    1662
Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
330             335             340             345
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```
aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc    1710
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val
            350             355             360
```

```
cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc    1758
Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly
            365             370             375
```

```
atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg    1806
Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val
            380             385             390
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```
gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg    1854
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg
            395             400             405
```

```
agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca    1902
Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala
410             415             420             425
```

```
gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac    1950
Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp
            430             435             440
```

```
tgg atc cac gag cag atg gag aga gac cta aaa acc tgaaaaggaa         1996
Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr
            445             450
```

```
gggacaagt agccacctga gttcctgagg tgatgaagac agcccgatcc tcccctggac    2056
tcccgtgtag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt    2116
agcaggcccg aaagaggcac ccttccatct gattccagca caaccttcaa gctgcttttt    2176
gttttttgtt tttttgagat ggagtctcgc tctgttgccc aggctggagt gcagtggcga    2236
aatccctgct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc    2296
cccagtagct gggaccacag gtgcccgcca ccacacccaa ctaattttttg tatttttagt    2356
agagacaggg tttcaccatg ttggccaggc tgctctcaaa cccctgacct caaatgatgt    2416
gcctgcttca gcctcccaca gtgctgggat tacaggcatg gccaccacg cctagcctca    2476
cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg gcggcctttc    2536
ccactggtcc atctggtttt ctctccaggg gtcttgcaaa attcctgacg agataagcag    2596
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ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga   2656
agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aacccaccct   2716
ttctacttcc aagacttatt ttcacatgtg gggaggttaa tctaggaatg actcgtttaa   2776
ggcctatttt catgatttct ttgtagcatt tggtgcttga cgtattattg tcctttgatt   2836
ccaaataata tgtttccttc cctcatwraa maaaaaaaaa aaaaaaaarr rmrrssgcta   2896
vavmarktta gagaaaaaac ctacccacrc cttcccctg aamctraaam ya           2948
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<210> 2
<211> 453
<212> PRT
<213> Homo sapiens

<400> 2

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Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg
 1               5                  10                  15
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
                20                  25                  30
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
            35                  40                  45
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
        50                  55                  60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
65                  70                  75                  80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
                85                  90                  95
Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
               100                 105                 110
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
           115                 120                 125
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
       130                 135                 140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
145                 150                 155                 160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
                165                 170                 175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
               180                 185                 190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
           195                 200                 205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
       210                 215                 220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
225                 230                 235                 240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
                245                 250                 255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
               260                 265                 270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
           275                 280                 285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
       290                 295                 300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
305                 310                 315                 320
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
                325                 330                 335
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
               340                 345                 350
```

```
Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
        355             360             365
Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
        370             375             380
Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
385             390             395             400
Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
                405             410             415
Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
                420             425             430
Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
        435             440             445
Arg Asp Leu Lys Thr
        450
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<210> 3
<211> 1362
<212> DNA
<213> Homo sapiens

<400> 3
atgggggaaa atgatccgcc tgctgttgaa gcccccttct cattccgatc gctttttggc      60
cttgatgatt tgaaaataag tcctgttgca ccagatgcag atgctgttgc tgcacagatc     120
ctgtcactgc tgccattgaa gttttttcca atcatcgtca ttgggatcat tgcattgata     180
ttagcactgg ccattggtct gggcatccac ttcgactgct cagggaagta cagatgtcgc     240
tcatccttta agtgtatcga gctgatagct cgatgtgacg gagtctcgga ttgcaaagac     300
ggggaggacg agtaccgctg tgtccgggtg ggtggtcaga atgccgtgct ccaggtgttc     360
acagctgctt cgtggaagac catgtgctcc gatgactgga agggtcacta cgcaaatgtt     420
gcctgtgccc aactgggttt cccaagctat gtgagttcag ataacctcag agtgagctcg     480
ctggaggggc agttccggga ggagtttgtg tccatcgatc acctcttgcc agatgacaag     540
gtgactgcat acaccactc agtatatgtg agggagggat gtgcctctgg ccacgtggtt      600
accttgcagt gcacagcctg tggtcataga aggggctaca gctcacgcat cgtgggtgga     660
aacatgtcct tgctctcgca gtggccctgg caggccagcc ttcagttcca gggctaccac     720
ctgtgcgggg gctctgtcat cacgcccctg tggatcatca ctgctgcaca ctgtgtttat     780
gacttgtacc tccccaagtc atggaccatc caggtgggtc tagtttccct gttggacaat     840
ccagccccat cccacttggt ggagaagatt gtctaccaca gcaagtacaa gccaaagagg     900
ctgggcaatg acatcgccct tatgaagctg ccgggccac tcacgttcaa tgaaatgatc      960
cagcctgtgt gcctgcccaa ctctgaagag aacttccccg atggaaaagt gtgctggacg    1020
tcaggatggg gggccacaga ggatggaggt gacgcctccc ctgtcctgaa ccacgcggcc    1080
gtccctttga tttccaacaa gatctgcaac acagggacg tgtacggtgg catcatctcc     1140
ccctccatgc tctgcgcggg ctacctgacg ggtggcgtgg acagctgcca ggggggacagc   1200
gggggcccc tggtgtgtca agagaggagg ctgtggaagt tagtgggagc gaccagcttt     1260
ggcatcggct cgcagaggt gaacaagcct ggggtgtaca cccgtgtcac ctccttcctg    1320
gactggatcc acgagcagat ggagagagac ctaaaaacct ga                       1362
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<210> 4
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 4
Ile Val Gly Gly Arg Glu Ala Gln Pro Gly Ser Phe Gly Ser Pro Trp
1               5               10              15
Gln Val Ser Leu Gln Val Arg Ser Gly Gly Gly Ser Arg Lys His Phe
```

```
                     20                        25                        30
Cys Gly Gly Ser Leu Ile Ser Glu Asn Trp Val Leu Thr Ala Ala His
        35                        40                        45
Cys Val Ser Gly Ala Ala Ser Ala Pro Ala Ser Ser Val Arg Val Ser
    50                        55                        60
Leu Ser Arg Val Arg Leu Gly Glu His Asn Leu Ser Leu Thr Glu Gly
65                        70                        75                        80
Thr Glu Gln Lys Phe Asp Val Lys Lys Thr Ile Ile Val His Pro Asn
                    85                        90                        95
Tyr Asn Pro Asp Thr Leu Asp Asn Gly Ala Tyr Asp Asn Asp Ile Ala
                100                       105                       110
Leu Leu Lys Leu Lys Ser Pro Gly Val Thr Leu Gly Asp Thr Val Arg
            115                       120                       125
Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp Leu Pro Val Gly Thr Thr
        130                       135                       140
Cys Thr Val Ser Gly Trp Gly Arg Arg Pro Thr Lys Asn Leu Gly Leu
145                       150                       155                       160
Ser Asp Thr Leu Gln Glu Val Val Val Pro Val Val Ser Arg Glu Thr
                165                       170                       175
Cys Arg Ser Ala Tyr Glu Tyr Gly Gly Thr Asp Asp Lys Val Glu Phe
                180                       185                       190
Val Thr Asp Asn Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala
                195                       200                       205
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Asn Arg
            210                       215                       220
Asp Gly Arg Trp Glu Leu Val Gly Ile Val Ser Trp Gly Ser Tyr Gly
225                       230                       235                       240
Cys Ala Arg Gly Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr
                    245                       250                       255
Leu Asp Trp Ile
                260


<210> 5
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 5
Arg Ile Val Gly Gly Ser Glu Ala Lys Ile Gly Ser Phe Pro Trp Gln
  1               5                        10                        15
Val Ser Leu Gln Cys Gly Gly Ser Leu Ile Ser Pro Arg Trp Val Leu
                20                        25                        30
Thr Ala Ala His Cys Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
        35                        40                        45
Gly Glu Glu Thr Glu Gly Gly Pro Arg Leu Asp Ser Pro Gly Gly Gln
    50                        55                        60
Val Ile Lys Val Ser Lys Ile Ile Glu Val His Pro Asn Tyr Asn Asn
65                        70                        75                        80
Asp Ile Ala Leu Leu Lys Leu Lys Glu Pro Val Thr Leu Ser Asp Ser
                    85                        90                        95
Asn Thr Val Arg Pro Ile Cys Leu Pro Ser Ser Asn Glu Ile Lys Thr
                100                       105                       110
Ser Glu Gly Asn Thr Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
            115                       120                       125
```

Trp Gly Arg Thr Ser Glu Gly Pro Glu Glu Ser Gly Gly Gly Ser Leu
    130   135   140
Pro Asp Val Leu Gln Glu Val Asn Val Pro Ile Val Ser Asn Glu Thr
145   150   155   160
Cys Arg Met Leu Cys Ala Gly Tyr Leu Glu Gly Gly Asn Thr Pro Gly
                165   170   175
Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Val
            180   185   190
Leu Val Gly Ile Val Ser Trp Gly Ser Ser Ser Leu Tyr Gly Cys Ala
        195   200   205
Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr Leu Asp
    210   215   220
Trp Ile
225

<210> 6
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 6
Ser Thr Cys Gly Gly Pro Asp Glu Phe Gln Cys Gly Ser Gly Arg Arg
1   5   10   15
Cys Ile Pro Arg Ser Trp Val Cys Asp Gly Asp Pro Asp Cys Glu Asp
            20   25   30
Gly Ser Asp Glu Ser Leu Glu Asn Cys Ala Ala
        35   40

<210> 7
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 7
Val Gly Gly Ser Ser Arg Cys Glu Gly Arg Val Glu Val Arg His Asp
1   5   10   15
Gly Ser Lys Trp Gly Thr Val Cys Asp Ser Ser Trp Ser Leu Arg Asp
            20   25   30
Ala Asn Val Asp Pro Gln Ala Ser Lys Val Cys Arg Gln Leu Gly Cys
        35   40   45
Gly Gly Ala Val Ser Leu Leu Gly Pro Tyr Phe Ser Glu Gly Gly Gly
    50   55   60
Pro Ala Gly Gln Arg Glu Ile Trp Leu Asp Gly Val Asn Cys Ser Gly
65   70   75   80
Asn Glu Thr Ser Leu Ser Gln Cys Pro Val Arg Val Thr Pro Pro Gly
                85   90   95
Leu Ser Arg Gln Cys Ser His Asp Gly Glu Asp Ala Gly Val Val Cys
            100   105   110
Ser

<210> 8
<211> 5
<212> PRT
<213> Homo sapiens

<400> 8
Arg Ile Val Gly Gly
 1   5

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<221> VARIANT
<222> 2
<223> Xaa = Asp or Glu

<221> VARIANT
<222> 5
<223> Xaa = Gly or Ser

<400> 9
Gly Xaa Ser Gly Xaa
 1   5

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<221> VARIANT
<222> 1
<223> Xaa = Leu, Ile, Val, or Met

<221> VARIANT
<222> 2
<223> Xaa = Ser or Thr

<221> VARIANT
<222> 4
<223> Xaa = Ser, Thr, Ala, or Gly

<400> 10
Xaa Xaa Ala Xaa His Cys
 1   5

<210> 11
<211> 2951
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (628)...(1989)

<221> misc_feature
<222> (1)...(2951)
<223> n = A,T,C or G

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gtatttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact     180
gttacccact ttgcctcgtc ttcaccctgt ccaaacaccg gtctccaatt tgcccttcag     240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca     300
ttatgttggc caacagaact tgattgtaaa aataataaa gaaatctgtt atatactttc      360
caaactccaa aaaaaaccg gaattcagcc tggttaagtc caagctgaat tccgggtggg      420
ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattaggtc atgcccgtat     480
gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc     540
gtggtgccat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg     600
gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt     654
                                Met Gly Glu Asn Asp Pro Pro Ala Val
                                 1               5

gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa      702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10              15                  20                  25

ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg      750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
             30                  35                  40

tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att      798
Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
         45                  50                  55

gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc      846
Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys
         60                  65                  70

tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata      894
Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile
     75                  80                  85

gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac      942
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 90              95                  100                 105

cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca      990
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr
                 110                 115                 120

gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac     1038
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr
             125                 130                 135

gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca     1086
```

Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser
        140   145   150

gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt   1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe
        155   160   165

gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac   1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His
170   175   180   185

cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc   1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr
                    190   195   200

ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc   1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile
            205   210   215

gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc   1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser
            220   225   230

ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc   1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro
            235   240   245

ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc   1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro
250   255   260   265

aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca   1470
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro
                    270   275   280

gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag   1518
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys
                285   290   295

cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca   1566
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro
            300   305   310

ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa   1614
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
            315   320   325

gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc   1662
Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
330   335   340   345

aca gag gat gga gca ggt gac gcc tcc cct gtc ctg aac cac gcg gcc   1710
Thr Glu Asp Gly Ala Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala
                    350   355   360

gtc cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt   1758
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly

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                365                      370                      375

ggc atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc    1806
Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly
            380                 385                 390

gtg gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag    1854
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu
            395                 400                 405

agg agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc    1902
Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys
410                 415                 420                 425

gca gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg    1950
Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu
                430                 435                 440

gac tgg atc cac gag cag atg gag aga gac cta aaa acc tgaagaggaa     1999
Asp Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr
                445                 450
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ggggacaagt agccacctga gttcctgagg tgatgaagac agcccgatcc tcccctggac    2059
tcccgtgtag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt    2119
agcaggcccg aaagaggcac ccttccatct gattccagca caaccttcaa gctgcttttt    2179
gttttttgtt ttttgagat ggagtctcgc tctgttgccc aggctggagt gcagtggcga    2239
aatccctgct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc    2299
cccagtagct gggaccacag gtgcccgcca ccacacccaa ctaattttttg tatttttagt    2359
agagacaggg tttcaccatg ttggccaggc tgctctcaaa cccctgacct caaatgatgt    2419
gcctgcttca gcctcccaca gtgctgggat tacaggcatg ggccaccacg cctagcctca    2479
cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg gcggcctttc    2539
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ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga    2659
agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aacccaccct    2719
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ggcctatttt catgatttct ttgtagcatt tggtgcttga cgtattattg tcctttgatt    2839
ccaaataata tgtttccttc cctcatwraa maaaaaaaa aaaaaaaarr rmrrssgcta    2899
vavmarktta gagaaaaaac ctacccacrc cttcccctg aamctraaam ya            2951
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<210> 12
<211> 454
<212> PRT
<213> Homo sapiens

<400> 12
Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg
1               5                   10                  15
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
            20                  25                  30
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Pro Leu Lys Phe
        35                  40                  45
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
    50                  55                  60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
65                  70                  75                  80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
                85                  90                  95
```

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Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
            100                 105             110
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
            115                 120             125
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
            130                 135             140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
145                 150                 155                 160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
                165                 170                 175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
                180                 185                 190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
            195                 200                 205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
            210                 215                 220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
225                 230                 235                 240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
                245                 250                 255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
                260                 265                 270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
            275                 280                 285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
            290                 295                 300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
305                 310                 315                 320
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
                325                 330                 335
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Ala Gly Asp
                340                 345                 350
Ala Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys
            355                 360                 365
Ile Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met
    370                 375                 380
Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp
385                 390                 395                 400
Ser Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val
                405                 410                 415
Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly
            420                 425                 430
Val Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met
            435                 440                 445
Glu Arg Asp Leu Lys Thr
450
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<210> 13
<211> 1365
<212> DNA
<213> Homo sapiens

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cttgatgatt tgaaaataag tcctgttgca ccagatgcag atgctgttgc tgcacagatc     120
ctgtcactgc tgccattgaa gttttttcca atcatcgtca ttgggatcat tgcattgata     180
ttagcactgg ccattggtct gggcatccac ttcgactgct cagggaagta cagatgtcgc     240
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tcatccttta agtgtatcga gctgatagct cgatgtgacg gagtctcgga ttgcaaagac    300
ggggaggacg agtaccgctg tgtccgggtg ggtggtcaga atgccgtgct ccaggtgttc    360
acagctgctt cgtggaagac catgtgctcc gatgactgga agggtcacta cgcaaatgtt    420
gcctgtgccc aactgggttt cccaagctat gtgagttcag ataacctcag agtgagctcg    480
ctggaggggc agttccggga ggagtttgtg tccatcgatc acctcttgcc agatgacaag    540
gtgactgcat tacaccactc agtatatgtg agggagggat gtgcctctgg ccacgtggtt    600
accttgcagt gcacagcctg tggtcataga aggggctaca gctcacgcat cgtgggtgga    660
aacatgtcct tgctctcgca gtggccctgg caggccagcc ttcagttcca gggctaccac    720
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gacttgtacc tccccaagtc atggaccatc caggtgggtc tagtttccct gttggacaat    840
ccagccccat cccacttggt ggagaagatt gtctaccaca gcaagtacaa gccaaagagg    900
ctgggcaatg acatcgccct tatgaagctg gccgggccac tcacgttcaa tgaaatgatc    960
cagcctgtgt gcctgcccaa ctctgaagag aacttccccg atggaaaagt gtgctggacg   1020
tcaggatggg gggccacaga ggatggagca ggtgacgcct cccctgtcct gaaccacgcg   1080
gccgtccctt tgatttccaa caagatctgc aaccacaggg acgtgtacgg tggcatcatc   1140
tccccctcca tgctctgcgc gggctacctg acgggtggcg tggacagctg ccaggggac   1200
agcggggggc ccctggtgtg tcaagagagg aggctgtgga agttagtggg agcgaccagc   1260
tttggcatcg gctgcgcaga ggtgaacaag cctggggtgt acaccgtgt cacctccttc   1320
ctggactgga tccacgagca gatggagaga gacctaaaaa cctga                   1365
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